SEQUENCE LISTING

<110> Lim, Moon Young
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Starr, Douglas B.
Laurance, Megan E.
Kwok, Yan

<120> DNA Binding Compound-Mediated Molecular Switch System

<130> 54600-8130.US00

<140> US 09/518,297
<141> 2000-03-03

<150> US 60/122,513
<151> 1999-03-03

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<151> 1999-09-17

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<223> transcriptional regulatory protein

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Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
35 40 45
Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
50 55 60
Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
65 70 75 80
Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
85 90 95
Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
100 105 110
Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
115 120 125
Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
130 135 140
Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
145 150 155 160
Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
165 170 175
Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
180 185 190
Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
195 200 205
Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
210 215 220
Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
225 230 235 240
Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
245 250 255
Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu
260 265 270
Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr
275 280 285
Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg
290 295 300
Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly

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305                 310                 315                 320
Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg
                325                 330                 335
Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr
            340                 345                 350
Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe
        355                 360                 365
Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro
    370                 375                 380
Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val
385                 390                 395                 400
Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly
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Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
            420                 425                 430
Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
        435                 440                 445
Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
    450                 455                 460
Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
465                 470                 475                 480
Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
                485                 490                 495
Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
            500                 505                 510
Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
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Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
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Leu Leu Ser Gln Ile Ser Ser
545                 550
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<220>
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<400> 6
cttaacactc gcgagtgtta ag 22

<210> 7
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rgntcantga cny 13

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<210> 9

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1 5 10 15
Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
20 25 30
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
35 40 45
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
50 55 60
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
65 70 75 80
Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
85 90 95
Val

<210> 11
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
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Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
 1   5   10   15
Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
            20   25   30
Met Leu Pro Tyr
        35

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<211> 116
<212> DNA
<213> Escherichia coli

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<222> (0)...(0)
<223> partial promoter sequence

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gccaccactg acacggaaca acggcaaaca cgccgccggg tcagcggggt tctcct 116

<210> 13
<211> 22
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (0)...(0)
<223> partial promoter sequence

<400> 13
agaaaattat tttaaatttc ct 22

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 14
gactgcagtg gtacctagga gg 22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 15
agaaaattat tttaaatttc ct 22

<210> 16

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence

<400> 16
ggaaaatttt ttttcaaaag ta 22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<400> 17
tgaaatttat tttgcgaaag gg 22

<210> 18
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 18
tgttcgcact t 11

<210> 19
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
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catggacgcc actgagccgt ttttgttcgc acttgaggcg agtcgatgca cc 52

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<211> 54
<212> DNA
<213> Artificial Sequence

<220>
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<400> 20
catggacgcc actgagccgt gttcgcactt ttttttgagg cgagtcgatg cacc 54

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<211> 58
<212> DNA
<213> Artificial Sequence

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<400> 21
catggacgcc actgagccgt ttttgttcgc actttttttt gaggcgagtc gatgcacc 58

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<220>
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<400> 22
cttaaaaata ac 12

<210> 23
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 23
ttgaaaaatc aacgct 16

<210> 24
<211> 21
<212> DNA
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<220>
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<400> 24
tttttgttcg cactttttt t 21

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<220>
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<400> 25
tttttgggat tttccttttt 20

<210> 26
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<220>
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<400> 26

aaaaaattgt gagcgctcac aatttttt 28

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acttta 6

<210> 28
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<400> 28
taccgacat 9

<210> 29
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<400> 29
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<400> 30
gggattttcc 10

<210> 31
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
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<400> 32
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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

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<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 34
aaaaaattgt gagcgctcac aatttttt 28

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<400> 35
ttttttttgt gagcggataa caaaa 25

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<220>
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<400> 36
tctgggatcc 10

<210> 37
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
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<400> 37
gagtttttt taag 14

<210> 38
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 38
gagttttaaa agag 14

<210> 39
<211> 969
<212> PRT
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<223> transcriptional regulatory protein

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Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val Phe Gln
20 25 30
Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu
35 40 45
Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
50 55 60
Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
65 70 75 80
Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
85 90 95
Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
100 105 110
Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala
115 120 125
Gly Pro Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His
130 135 140
Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
145 150 155 160
Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu
165 170 175
Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly Asp Arg
180 185 190
Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met
195 200 205
Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
210 215 220
Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
225 230 235 240
Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met

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Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
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Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
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Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
    290                 295                 300
Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
305                 310                 315                 320
Asp Ile Asn Ile Thr Lys Pro Ala Ser Val Phe Val Gln Leu Arg Arg
                325                 330                 335
Lys Ser Asp Leu Glu Thr Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro
            340                 345                 350
Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg Gln Lys Leu Met
        355                 360                 365
Pro Asn Phe Ser Asp Ser Phe Gly Gly Gly Ser Gly Ala Gly Ala Gly
    370                 375                 380
Gly Gly Gly Met Phe Gly Ser Gly Gly Gly Gly Gly Gly Thr Gly Ser
385                 390                 395                 400
Thr Gly Pro Gly Tyr Ser Phe Pro His Tyr Gly Phe Pro Thr Tyr Gly
                405                 410                 415
Gly Ile Thr Phe His Pro Gly Thr Thr Lys Ser Asn Ala Gly Met Lys
            420                 425                 430
His Gly Thr Met Asp Thr Glu Ser Lys Lys Asp Pro Glu Gly Cys Asp
        435                 440                 445
Lys Ser Asp Asp Lys Asn Thr Val Asn Leu Phe Gly Lys Val Ile Glu
    450                 455                 460
Thr Thr Glu Gln Asp Gln Glu Pro Ser Glu Ala Thr Val Gly Asn Gly
465                 470                 475                 480
Glu Val Thr Leu Thr Tyr Ala Thr Gly Thr Lys Glu Glu Ser Ala Gly
                485                 490                 495
Val Gln Asp Asn Leu Phe Leu Glu Lys Ala Met Gln Leu Ala Lys Arg
            500                 505                 510
His Ala Asn Ala Leu Phe Asp Tyr Ala Val Thr Gly Asp Val Lys Met
        515                 520                 525
Leu Leu Ala Val Gln Arg His Leu Thr Ala Val Gln Asp Glu Asn Gly
    530                 535                 540
Asp Ser Val Leu His Leu Ala Ile Ile His Leu His Ser Gln Leu Val
545                 550                 555                 560
Arg Asp Leu Leu Glu Val Thr Ser Gly Leu Ile Ser Asp Asp Ile Ile
                565                 570                 575
Asn Met Arg Asn Asp Leu Tyr Gln Thr Pro Leu His Leu Ala Val Ile
            580                 585                 590
Thr Lys Gln Glu Asp Val Val Glu Asp Leu Leu Arg Ala Gly Ala Asp
        595                 600                 605
Leu Ser Leu Leu Asp Arg Leu Gly Asn Ser Val Leu His Leu Ala Ala
    610                 615                 620
Lys Glu Gly His Asp Lys Val Leu Ser Ile Leu Leu Lys His Lys Lys
625                 630                 635                 640
Ala Ala Leu Leu Leu Asp His Pro Asn Gly Asp Gly Leu Asn Ala Ile
                645                 650                 655
His Leu Ala Met Met Ser Asn Ser Leu Pro Cys Leu Leu Leu Leu Val
            660                 665                 670
Ala Ala Gly Ala Asp Val Asn Ala Gln Glu Gln Lys Ser Gly Arg Thr
        675                 680                 685
Ala Leu His Leu Ala Val Glu His Asp Asn Ile Ser Leu Ala Gly Cys
    690                 695                 700
Leu Leu Leu Glu Gly Asp Ala His Val Asp Ser Thr Thr Tyr Asp Gly
705                 710                 715                 720
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Thr Thr Pro Leu His Ile Ala Ala Gly Arg Gly Ser Thr Arg Leu Ala
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Ala Leu Leu Lys Ala Ala Gly Ala Asp Pro Leu Val Glu Asn Phe Glu
            740                 745                 750
Pro Leu Tyr Asp Leu Asp Asp Ser Trp Glu Asn Ala Gly Glu Asp Glu
        755                 760                 765
Gly Val Val Pro Gly Thr Thr Pro Leu Asp Met Ala Thr Ser Trp Gln
    770                 775                 780
Val Phe Asp Ile Leu Asn Gly Lys Pro Tyr Glu Pro Glu Phe Thr Ser
785                 790                 795                 800
Asp Asp Leu Leu Ala Gln Gly Asp Met Lys Gln Leu Ala Glu Asp Val
                805                 810                 815
Lys Leu Gln Leu Tyr Lys Leu Leu Glu Ile Pro Asp Pro Asp Lys Asn
            820                 825                 830
Trp Ala Thr Leu Ala Gln Lys Leu Gly Leu Gly Ile Leu Asn Asn Ala
        835                 840                 845
Phe Arg Leu Ser Pro Ala Pro Ser Lys Thr Leu Met Asp Asn Tyr Glu
    850                 855                 860
Val Ser Gly Gly Thr Val Arg Glu Leu Val Glu Ala Leu Arg Gln Met
865                 870                 875                 880
Gly Tyr Thr Glu Ala Ile Glu Val Ile Gln Ala Ala Ser Ser Pro Val
                885                 890                 895
Lys Thr Thr Ser Gln Ala His Ser Leu Pro Leu Ser Pro Ala Ser Thr
            900                 905                 910
Arg Gln Gln Ile Asp Glu Leu Arg Asp Ser Asp Ser Val Cys Asp Thr
        915                 920                 925
Gly Val Glu Thr Ser Phe Arg Lys Leu Ser Phe Thr Glu Ser Leu Thr
    930                 935                 940
Ser Gly Ala Ser Leu Leu Thr Leu Asn Lys Met Pro His Asp Tyr Gly
945                 950                 955                 960
Gln Glu Gly Pro Leu Glu Gly Lys Ile
                965
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<220>
<223> engineered regulatory sequence

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agcagagctc gtttagtgaa ccgtcagatc agatct 96

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<211> 154
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 41
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atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg tttatataag 120
cagagctcgt ttagtgaacc gtcagatcag atct 154

<210> 42

<211> 212
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 42
acgcgtgccc aaattgggat tttccaaaaa gccgaaattg ggattttcca aaaaccgcgc 60
tagcgcccaa attgggattt tccaaaaagc cgaaattggg attttccaaa aaccgccgat 120
cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt tatataagca 180
gagctcgttt agtgaaccgt cagatcagat ct 212

<210> 43
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 43
gctagccccg ccccgttgac gcaaatgggc ggtaggcgtg tacggtggga ggtctatata 60
agcagagctc gtttagtgaa ccgtcagatc agatct 96

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gctagcgccc aggtcgggat tttccgagga gccgaggtcg ggattttccg aggaccgccg 60
atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag 120
cagagctcgt ttagtgaacc gtcagatcag atct 154

<210> 45
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<213> Artificial Sequence

<220>
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atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag 120
cagagctcgt ttagtgaacc gtcagatcag atct 154

<210> 46
<211> 762
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct

<400> 46
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tggctattgg ccattgcata cgttgtatct atatcataat atgtacattt atattggctc 120
atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat 180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240
tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 300
tcccatagta acgcaaatag ggattttcca ttaacgtcaa tgggtggagt atttacggta 360
aactgcccac ttggcagtac atcaagtgta tcatatgcca agtccgcccc ctattgacgt 420
caatgacggt aaatggcccg cctggcatta tgcccagtac atgactttat gggattttcc 480
tatttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggttttggca 540
gtacaccaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat 600
tgacgtcaat gggagtttgt tttggcacca aggtaaaagg gattttccaa aatgtcgtaa 660
caactgcgat cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt 720
tatataagca gagctcgttt agtgaaccgt cagatcaagc tt 762

<210> 47
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<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct

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tggctattgg ccattgcata cgttgtatct atatcataat atgtacattt atattggctc 120
atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat 180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240
tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 300
tcccatagta acgcaaatat tcccgggaaa ttaacgtcaa tgggtggagt atttacggta 360
aactgcccac ttggcagtac atcaagtgta tcatatgcca agtccgcccc ctattgacgt 420
caatgacggt aaatggcccg cctggcatta tgcccagtac atgactttat tctcgaggaa 480
tatttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggttttggca 540
gtacaccaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat 600
tgacgtcaat gggagtttgt tttggcacca aggtaaaatt acgcgtaaaa aatgtcgtaa 660
caactgcgat cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt 720
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<212> DNA
<213> Artificial Sequence

<220>
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atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat 180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa 240
tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt 300
tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggagt atttacggta 360
aactgcccac ttggcagtac atcaagtgta tcatatgcca agtccgcccc ctattgacgt 420
caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttac gggactttcc 480
tacttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggttttggca 540
gtacaccaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat 600
tgacgtcaat gggagtttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 660
caactgcgat cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtc 720

tatataagca gagctcgttt agtgaaccgt cagatcaagc tt 762

<210> 49
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> wild type regulatory sequence

<400> 49
gactgtttgt tt 12

<210> 50
<211> 12
<212> DNA
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<220>
<223> wild type regulatory sequence

<400> 50
aggactcttg ga 12

<210> 51
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> wild type regulatory sequence

<400> 51
tactaggagg ctgtaggcat aaattggtct gcgcaccagc accatg 46

<210> 52
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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